# CNN - Based Cell Detector

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SSY097 Image analysis

## Objectives

The objective of the project is to train a fully convolutional neural network *(CNN)* to detect and count blood cells in a microscopic image.

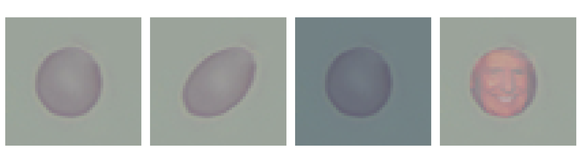
## Overview

A convolutional neural network takes in an arbitrarily large patch from an image and ouputs a single pixel response. The value of the response is the probability of the input patch being an image which the network is trained to detect.

## Data augmentation

The amount of data available to train the network is an important factor in how well the network will detect the cells in the image. To get the most out of the available training data it's good to augment it, i.e. take the available training data and skew it a little bit.

The operations used in this assignment to augment the data were: translation, affine warping, rescaling, noise addition, change of contrast and gaussian smoothing. Moreover, random augmentations were done on each sample and the number of augmentations done on each sample were also chosen at random for each sample.



Original Skew Contrast Distort

## Training on hard data

To increase the accuracy, hard examples were extracted from the training set and saved between each iteration. The algorithm does some iterations of the hard data set when at least 300 hard samples has been extracted and then does it at random with an increasing probability if it has not been done for a while. As can be seen in 1 this makes the number of miss classifications more stable later on in the iterations.

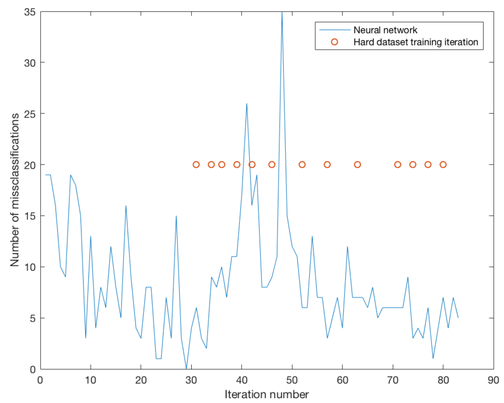



Figure 1: Number of missclassifications for each iteration that are added to the hard dataset

## Sub pixel precision

When determining where each cell center lies the outputted probability map is max filtered so that the pixel with the highest probability is selected as the cell center. However it's likely that the true maxima lies somewhere in between the pixels. Using Taylor expansion to estimate the gradient around the cell center it is possible to refine the position of the cell center and thus getting *sub pixel precision*.
The Taylor expansion is as follows:

$$\begin{bmatrix} x \\ y \end{bmatrix} = -H^{-1}(0,0)\nabla f(0,0) \qquad (1)$$

where (x,y) is the sub pixel coordinate of the cell center and H(0,0) and $\nabla$f(0,0) are the Hessian and gradient estimates around the strict local maxima.

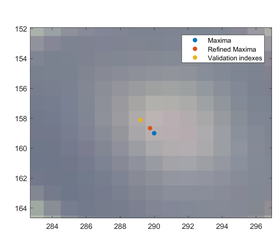



Figure 2: Sub pixel precision

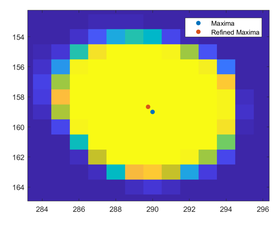



Figure 3: Sub pixel precision probability map

## Network validation

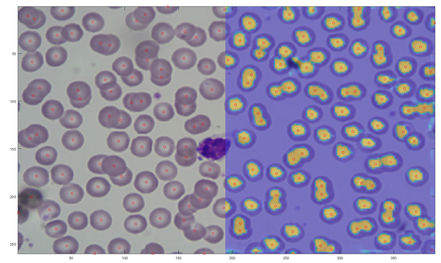


Figure 5: Probabilitymap for a trained network on a validation picture with the validation centers marked with red circles

The Euclidean distance between the correct and estimated cell centers was used to get an estimate on the network's accuracy. As can be seen from 1 the Euclidean distance decreases notably after running sub pixel precision on the estimated cell centers.

| **Validation image** | 1 | 2 | 3 |
|---|---|---|---|
| **Outliers** | 7 | 4 | 11 |
| **Residuals/inlier (non refined)** | 1.2739 | 2.1561 | 1.2191 |
| **Residuals/inlier (refined)** | 0.9243 | 1.8179 | 1.1715 |

Table 1: Network precision

## Layers

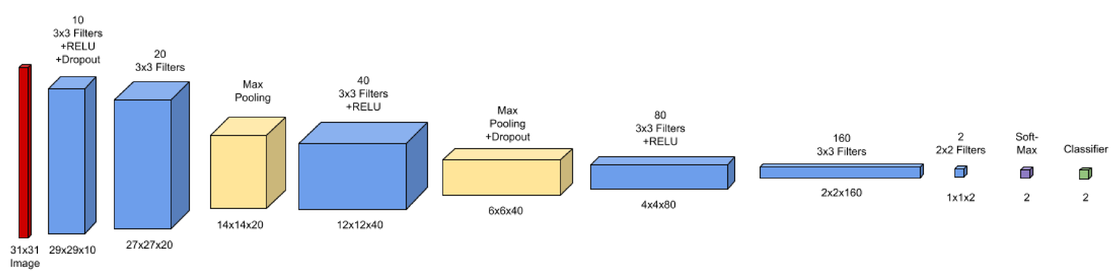



Figure 4: Graphic representation of the convolutional neural network

## Results

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